

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:08 ; Search time 88.16 seconds
(without alignments)
29.249 Million cell updates/sec

Title: US-09-331-631A-39

Perfect score: 54
Sequence: 1 CXXXXCXXXXXXXXXXXXCXXC 22

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	39	13	09PVG7
2	54	100.0	43	5	09VDN2
3	54	100.0	44	11	060620
4	54	100.0	46	4	016861
5	54	100.0	46	11	060622
6	54	100.0	47	5	09N9H0
7	54	100.0	49	5	023947
8	54	100.0	49	5	023948
9	54	100.0	49	13	042597
10	54	100.0	54	11	008636
11	54	100.0	57	5	09N9H2
12	54	100.0	58	5	09U623
13	54	100.0	59	5	09N9H1
14	54	100.0	62	10	065918
15	54	100.0	66	5	09VE14
16	54	100.0	67	6	09TSF0
17	54	100.0	68	5	002033
18	54	100.0	71	5	076957
19	54	100.0	72	5	09V199

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20	54	100.0	73	5	09U569	09U569 perna virid
21	54	100.0	73	5	09U568	09U568 perna virid
22	54	100.0	73	10	041615	041615 tradescanti
23	54	100.0	74	5	09V1A1	09V1A1 drosophila
24	54	100.0	75	5	09V388	09V388 perna virid
25	54	100.0	75	5	09XX96	09XX96 caenorhabdi
26	54	100.0	75	5	09UIN5	09UIN5 crassostrea
27	54	100.0	76	10	040855	040855 picea glauc
28	54	100.0	76	10	024155	024155 nicotiana t
29	54	100.0	77	5	076955	076955 lumbricus t
30	54	100.0	78	9	09T135	09T135 bacterioph
31	54	100.0	80	10	09SG42	09SG42 arabidopsis
32	54	100.0	83	11	09TMA5	09TMA5 mus musculu
33	54	100.0	84	13	090248	090248 bombyx mori
34	54	100.0	86	5	045833	045833 caenorhabdi
35	54	100.0	87	10	080641	080641 arabidopsis
36	54	100.0	88	4	09UKK0	09UKK0 homo sapien
37	54	100.0	89	11	088459	088459 mus musculu
38	54	100.0	90	5	045834	045834 caenorhabdi
39	54	100.0	91	10	049134	049134 fragaria an
40	54	100.0	95	10	041521	041521 trititum ae
41	54	100.0	97	5	09NEK7	09NEK7 caenorhabdi
42	54	100.0	97	10	038939	038939 arabidopsis
43	54	100.0	101	10	065313	065313 lavatera th
44	54	100.0	101	10	09XGJ3	09XGJ3 gerbera hyb
45	54	100.0	102	10	024040	024040 lavatera th

ALIGNMENTS

RESULT 1
09PVG7 PRELIMINARY; PRT: 39 AA.
AC 09PVG7;
DT 01-MAY-2000 (TREMBLrel..13, Created)
DT 01-MAY-2000 (TREMBLrel..13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel..13, Last annotation update)
DE RECEPTOR TYROSINE KINASE XMURK (FRAGMENT).
GN XMURK.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
XX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SR.
RA MEDLINE-99126443; PubMed-9927468;
RX Guldberg H., Scharf M.;
RT "Intergenic sex-chromosomal crossovers of Xmrk oncogene alleles affect
RT pigment pattern formation and the severity of melanoma in
RT Xiphophorus";
RL Genetics 151:773-783(1999).
DR EMBL; AF092693; AAD03714.1;
KW Receptor; Kinase.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA: 4195 MW; 42303BA05F6DB557 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 39;
Best Local Similarity 18.2%; Pred. NO. 71;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXCXXXXXXXXXXXXCXXC 22
[:::XXXXXXXXXXXXX:::]
DB 5 CAECNCRCRGRPRIDCCNEHC 26

RESULT 2
09VDN2

ID	Q9VDN2	PRELIMINARY;	PRT;	43 AA.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)			
DE	CG5097 PROTEIN.			
GN	CG5097.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Mananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yancelli M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,			
RA	April J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Berens P.V., Bertram B.P., Bhattacharya D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Mekulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of Drosophila melanogaster.";			
RL	Science 287:2185-2195(2000).			
DR	EMBL: AEO03730; AAF55758.1; -			
DR	FLYBASE: FBgn0038790; CG5097.			
DR	INTERPRO: IPR000561; -			
DR	INTERPRO: IPR000966; -			
DR	PFAM: PF02067; Metallothio_5; 1.			
DR	PRINTS: PRO0872; MTDIPTEA.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
QO	SEQUENCE 43 AA: 4597 MW: E54E722B14E89DDE CRC64;			

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Overy Match      100.0%; Score 54; DB 5; Length 43;  
Best Local Similarity    18.2%; Pred. No. 75;  
Matches      4; Conservative   0; Indels     0; Gaps     0;
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SEQUENCE	44 AA:	4892 MP:	59F2E69015593F8C CR664:
SO	NON_TER	44	44
ET	1	1	1
FT	1	1	1
DR	PROSITE: PS00427; DISINTEGRIN_1; 1.		
DR	PFAM: Pf00200; disintegrin; 1.		
DR	SMART: SM001762; -		
DR	MGD: MGI:105987; Adam32.		
DR	HSSD: P17347; 2ECH.		
DR	EMBL: U06147; AA18426.1; -.		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).		
RT	"A family of cellular proteins related to snake venom disintegrins."		
RA	Weekamp G., Blobel C.P.;		
KX	MEDLINE:94195820; PubMed-8146185;		
RC	STRAIN-BALB/C;		
RP	SEQUENCE FROM N.A.		
RN	[1]		
OX	NCBI_TaxID=10090;		
GN	ADAM32 OR DTGNG2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
DE	DISINTEGRIN 2 (CELLULAR DISINTEGRIN-RELATED PROTEIN) (FRAGMENT).		
DT	01-JUL-1997 (TREMBLrel. 04, last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)		
AC	Q06020;		
ID	Q06020	PRELIMINARY;	PRT; 44 AA.
REMARK	060620		

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Query Match Similarity      100.0%; Score 54; DB 11; Length 44;
Best Local Similarity      18.2%; Pred. No. 76;
Matches      4; Conservative      18; Mismatches      0; Indels      0; Gaps      0.

OY      1 CXXXCXXXXXXXXXXXXXCCXXC 22
      |::|::|::|::|::|::|::|::|
Db      9 CEPCTILKKDAECSHGLCCNNC 30

RESULT      4
O16861
ID      O16861      PRELIMINARY;      PRT;      46 AA.
AC      O16861:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE      CYSTEINE-RICH PROTEIN (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Lemasson I., Devaux C., Mesnard J.M.;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U63532; AAB05810.1; -.
FT      NMR_TER      1      1
FT      SEQUENCE      46 AA; 5061 MW; 311922FE40A44E8F CRC64;

Query Match      100.0%; Score 54; DB 4; Length 46;
Best Local Similarity      18.2%; Pred. No. 78;
Matches      4; Conservative      18; Mismatches      0; Indels      0; Gaps      0.

OY      1 CXXXCXXXXXXXXXXXXXCCXXC 22
      |::|::|::|::|::|::|::|::|
Db      11 CCCCCCCCCCCCCCCCCCCCCC 32

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RESULT	5
Q060622	
ID	Q060622
PRELIMINARY;	
PRT;	46 AA

AC Q060622;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE DISINTEGRIN 4 (CELLULAR DISINTEGRIN-RELATED PROTEIN) (FRAGMENT).
 GN ADAM26 OR DTGM4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C.
 RX MEDLINE-94195820; PubMed-8146185;
 RA Weskamp G., Blobel C.P.;
 RT "A family of cellular proteins related to snake venom disintegrins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).
 DR EMBL; 006149; AAA18428.1; -.
 DR HSSP; P18619; 1FVL.
 DR MGD; MGI:105985; Adam26.
 DR INTERPRO; IPR001762; -.
 DR PFM: PF00200; disintegrin; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 FT NON_TER 1
 FT SEQUENCE 46 AA; 4950 MW; 9E22D616D4B716AC CRC64;

Query Match 100.0%; Score 54; DB 11; Length 46;
 Best Local Similarity 18.2%; Pred. No. 78;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 11 CSDCVLKPACACFGLCKNC 32

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RESULT 6
 ID Q09N9H0 PRELIMINARY; PRT; 47 AA.
 AC Q09N9H0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METLLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Venerupis pullastra.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Venerupis.
 NCBI_TaxID=104387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanguy A.;
 RT "Characterisation of metallothionein sequences in three clams
 Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 pullastra.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249688; CAB96419.1; -.
 FT NON_TER 1
 FT SEQUENCE 47 AA; 4602 MW; 6FDD54B9126F2B4F CRC64;

Query Match 100.0%; Score 54; DB 5; Length 47;
 Best Local Similarity 18.2%; Pred. No. 79;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 11 CSDCPATGCKCGPCGCGC 32

RESULT 7
 ID Q23947 PRELIMINARY; PRT; 49 AA.
 AC Q23947;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHTC3.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuech A., Buemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41117.1; -.
 DR FLYBASE; FBgn0015096; Dhyd\Mst87Fa.
 DR INTERPRO; IPR001450; -.
 DR PROSITE; PS00198; 4FE4S_FERRDOXIN; UNKNOWN_1.
 DR SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 6 CGGCGPGCGCGPCSCGPGC 27

RESULT 8
 ID Q23948 PRELIMINARY; PRT; 49 AA.
 AC Q23948;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHTC2.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuech A., Buemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41118.1; -.
 DR FLYBASE; FBgn0015097; Dhyd\Mst87Fb.
 DR INTERPRO; IPR001450; -.
 DR PROSITE; PS00198; 4FE4S_FERRDOXIN; UNKNOWN_1.
 DR SEQUENCE 49 AA; 4550 MW; 24758FEC51369F1D CRC64;

Query Match 100.0%; Score 54; DB 5; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 6 CGGCGPGCGCGPCSCGPGC 27

RESULT 9
 ID 042597 PRELIMINARY; PRT; 49 AA.
 AC 042597;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DE 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE METALLOPROTEASE/DISINTEGRIN XMDCL1.1 (FRAGMENT).
 OC Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=97349132; PubMed=9205136;
 RA Shilling F.M., Kratzschmar J., Cai H., Weskamp G., Gayko U.,
 RA Leibold J., Myles D.G., Nuccitelli R., Blobel C.P.;
 RT "Identification of metalloprotease/disintegrins in Xenopus laevis
 RT testis with a potential role in fertilization.";
 RL Dev. Biol. 186:155-164(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Kratzschmar J., Cai H., Blobel C.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U78189; AAB87149.1; -;
 DR HSSP; P17494; 1KST.
 DR INTERPRO: IPR001762; -;
 DR PFAM; PF00200; disintegrin.1.
 KW Integrin; Protease; Metalloprotease.
 FT NON_TER 1
 FT SEQUENCE 49 AA; 5316 MW; EFBDAE74DA582609 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

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DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE HIGH-GLYCINE TYROSINE KERATIN TYPE II.3 (FRAGMENT).
 GN KRTAP6-3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RA Aoki N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D89901; BAA19687.1; -;
 DR MGD; MGI:1330279; Krtap6-3.
 KW Keratin.
 FT NON_TER 1
 FT SEQUENCE 54 AA; 5729 MW; 2E7880E8822C1787 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 54;
 Best Local Similarity 18.2%; Pred. No. 86;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 ID Q9N9H2 PRELIMINARY; PRT; 57 AA.
 AC Q9N9H2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes philippinarum.
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 CC Veneroidea; Veneridae; Ruditapes.
 NX NCBI_TaxID=104384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanquy A.;
 RT "Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 RT pullastra.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249686; CAB96403.1; -;
 FT NON_TER 1
 FT SEQUENCE 57 AA; 5411 MW; F7B37567623FD7DD CRC64;

Query Match 100.0%; Score 54; DB 5; Length 57;
 Best Local Similarity 18.2%; Pred. No. 88;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN.
 OS Pacifastacus leniusculus (Signal crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Astacidea; Astacidae; Pacifastacus.
 NX NCBI_TaxID=6720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THORACIC GANGLIA;
 RA Skorupski P., Dawbarn D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF199482; AAF07215.1; -;
 DR HSSP; P55949; 1DMC.
 DR INTERPRO: IPR002045; -;
 DR INTERPRO: IPR003019; -;
 DR PFAM; PF00131; metalchio.1.
 DR PRINTS; PR00858; MTCRUSTACEAN.
 FT NON_TER 1
 FT SEQUENCE 58 AA; 6008 MW; 576635ACFB0E5100 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 58;
 Best Local Similarity 18.2%; Pred. No. 89;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 ID 09N9H1 PRELIMINARY; PRT; 59 AA.
 AC 09N9H1:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes decussatus.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchita; Veneroidea;
 OC Veneroidea; Veneridae; Ruditapes.
 OC NCBI_TaxID=104385;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanguy A.;
 RT "Characterisation of metallothionein sequences in three classes of
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerup
 RT pullastra".
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ249687; CAB96402.1;
 FT NON_TER 1 50
 FT SEQUENCE 59 AA; 5613 MW; CAB87C9FE35EC8A2 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 59;
 Best Local Similarity 18.2%; Pred. No. 90;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXX
 ID 14 CSDSCPATGCKGCGKCGGCGC 35

RESULT 14
 ID 065918 PRELIMINARY; PRT; 62 AA.
 AC 065918:
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE GAS5-LIKE PROTEIN (FRAGMENT).
 GN SB35.
 OS Picea mariana (Black spruce).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Picea.
 OX NCBI_TaxID=3335;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Perry D.J., Bousquet J.;
 RL Genetics 0:0-0(1998).
 DR EMBL: AF051754; AAC32171.1;
 DR EMBL: AF051753; AAC32170.1;
 DR MENDEL: 29301; P1cma; 1249; 29301.
 FT NON_TER 1 1
 FT SEQUENCE 62 AA; 6886 MW; A576222C14631F35 CRC64;

Query Match 100.0%; Score 54; DB 10; Length 62;
 Best Local Similarity 18.2%; Pred. No. 93;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXX
 ID 4 CGGRCYSRCSATSHKKPCMFEC 25

RESULT 15
 ID 09VE14 PRELIMINARY; PRT; 66 AA.

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AC 09VE14:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG7606 PROTEIN.
 GN CG7606.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridiata; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bihamil D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal C.,
 RA Jabali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Le J., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paack J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington C., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003718; AAF5437.1;
 DR FLYBASE: FBgn040565; CG7606.
 SQ SEQUENCE 66 AA; 6812 MW; 8151AF9DB3BF85FC CRC64;

Query Match 100.0%; Score 54; DB 5; Length 66;
 Best Local Similarity 18.2%; Pred. No. 96;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXX
 ID 30 CGGCGCKPQCLSCGSRSCGCGC 51

Search completed: March 1, 2001, 16:22:09
 Job time: 286 sec

